

1646

RAW SEQUENCE LISTING      DATE: 11/28/2000  
 PATENT APPLICATION: US/08/900,220C      TIME: 11:51:02

Input Set : A:\ONV-044.01 SeqList.txt  
 Output Set: N:\CRF3\11282000\H900220C.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
 C--> 6 (i) APPLICANT: Miao, Ningning  
 7 Wang, Monica  
 8 Mahanthappa, Nagesh K.  
 9 Pang, Kevin  
 10 Jin, Ping  
 12 (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and  
 13 GABA-nergic Disorders  
 15 (iii) NUMBER OF SEQUENCES: 32  
 17 (iv) CORRESPONDENCE ADDRESS:  
 18 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 19 (B) STREET: ONE POST OFFICE SQUARE  
 20 (C) CITY: Boston  
 21 (D) STATE: MA  
 22 (E) COUNTRY: USA  
 23 (F) ZIP: 02109  
 25 (v) COMPUTER READABLE FORM:  
 26 (A) MEDIUM TYPE: Floppy disk  
 27 (B) COMPUTER: IBM PC compatible  
 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 29 (D) SOFTWARE: AscII (text)  
 31 (vi) CURRENT APPLICATION DATA:  
 C--> 32 (A) APPLICATION NUMBER: US/08/900,220C  
 C--> 33 (B) FILING DATE: 24-Jul-1997  
 34 (C) CLASSIFICATION:  
 36 (viii) ATTORNEY/AGENT INFORMATION:  
 37 (A) NAME: Vincent, Matthew P.  
 38 (B) REGISTRATION NUMBER: 36,709  
 39 (C) REFERENCE/DOCKET NUMBER: ONV-044.01  
 41 (ix) TELECOMMUNICATION INFORMATION:  
 42 (A) TELEPHONE: (617) 832-1000  
 43 (B) TELEFAX: (617) 832-7000  
 46 (2) INFORMATION FOR SEQ ID NO: 1:  
 47 (i) SEQUENCE CHARACTERISTICS:  
 48 (A) LENGTH: 1277 base pairs  
 49 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: both  
 51 (D) TOPOLOGY: linear  
 53 (ii) MOLECULE TYPE: cDNA  
 55 (ix) FEATURE:  
 56 (A) NAME/KEY: CDS  
 57 (B) LOCATION: 1..1275  
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 61 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC  
 62 Met Val Glu Met Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile  
 63 1 5 10 15

ENTERED

see p.5

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DEC 15 2000

TECH CENTER 1600/2900

#31

WZ

48

## RAW SEQUENCE LISTING

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Input Set : A:\ONV-044.01 SeqList.txt

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65	TGC	GCT	CTT	TTA	GTC	TCC	TCT	GGG	CTG	ACT	TGT	GGA	CCA	GGC	AGG	GGC	96
66	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly	
67			20					25					30				
69	ATT	GGA	AAA	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCG	TTA	GCC	TAT	AAG	144
70	Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
71			35					40					45				
73	CAG	TTT	ATT	CCC	AAT	GTG	GCA	GAG	AAG	ACC	CTA	GGG	GCC	AGT	GGA	AGA	192
74	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
75			50					55					60				
77	TAT	GAA	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAG	AGA	TTT	AAA	GAA	CTA	ACC	240
78	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
79		65				70				75				80			
81	CCA	AAT	TAC	AAC	CCT	GAC	ATT	ATT	TTT	AAG	GAT	GAA	GAG	AAC	ACG	GGA	288
82	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
83				85						90				95			
85	GCT	GAC	AGA	CTG	ATG	ACT	CAG	CGC	TGC	AAG	GAC	AAG	CTG	AAT	GCC	CTG	336
86	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	
87			100						105				110				
89	GCG	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGG	GTG	AAG	CTG	CGG	GTG	ACC	384
90	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
91			115					120					125				
93	GAG	GGC	TGG	GAC	GAG	GAT	GGC	CAT	CAC	TCC	GAG	GAA	TCG	CTG	CAC	TAC	432
94	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
95			130					135					140				
97	GAG	GGT	CGC	GCC	GTG	GAC	ATC	ACC	ACG	TCG	GAT	CGG	GAC	CGC	AGC	AAG	480
98	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	
99	145				150					155				160			
101	TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTC	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
102	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
103				165						170				175			
105	TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
106	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
107				180						185				190			
109	TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
110	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
111			195					200					205				
113	CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCT	GGG	672
114	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
115			210					215					220				
117	GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
118	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
119	225				230					235				240			
121	TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
122	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
123				245						250				255			
125	GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
126	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
127			260							265				270			
129	CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864

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130 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
131      275      280      285
133 TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA      912
134 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
135      290      295      300
137 CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT      960
138 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
139 305      310      315
141 GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA      1008
142 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
143      325      330      335
145 CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC      1056
146 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
147      340      345      350
149 TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA      1104
150 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
151      355      360      365
153 TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC      1152
154 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
155      370      375      380
157 ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG      1200
158 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
159 385      390      395      400
160 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT      1248
161 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
162      405      410      415
163 CCG CTG GCC ATG GTG GCA CCG GCC AGC TG      1277
164 Pro Leu Gly Met Val Ala Pro Ala Ser
165      420      425
168 (2) INFORMATION FOR SEQ ID NO: 2:
170 (i) SEQUENCE CHARACTERISTICS:
171 (A) LENGTH: 1190 base pairs
172 (B) TYPE: nucleic acid
173 (C) STRANDEDNESS: both
174 (D) TOPOLOGY: linear
176 (ii) MOLECULE TYPE: cDNA
178 (ix) FEATURE:
179 (A) NAME/KEY: CDS
180 (B) LOCATION: 1..1191
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
184 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG      48
185 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
186 1      5      10      15
188 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG      96
189 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
190      20      25      30
192 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT      144
193 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
194      35      40      45

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RAW SEQUENCE LISTING                      DATE: 11/28/2000  
 PATENT APPLICATION: US/08/900,220C                      TIME: 11:51:02

Input Set : A:\ONV-044.01 SeqList.txt  
 Output Set: N:\CRF3\11282000\H900220C.raw

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196 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG      192
197 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
198      50                      55                      60
200 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC      240
201 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
202 65                      70                      75                      80
204 TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC      288
205 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
206      85                      90                      95
208 CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC      336
209 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
210      100                     105                     110
212 GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC      384
213 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
214      115                     120                     125
216 TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC      432
217 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
218      130                     135                     140
220 CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT      480
221 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
222 145                     150                     155                     160
224 TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC      528
225 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
226      165                     170                     175
228 GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG      576
229 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
230      180                     185                     190
232 GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG      624
233 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
234      195                     200                     205
236 CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG      672
237 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
238      210                     215                     220
240 GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG      720
241 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
242 225                     230                     235                     240
244 CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG      768
245 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
246      245                     250                     255
248 GAG ACC GAG CGG CCT CCG CGC AAA CTG TTG CTC ACA CCC TGG CAT CTG      816
249 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
250      260                     265                     270
252 GTG TTC GCT GCT CGC GGG CCA GCG CCT GCT CCA GGT GAC TTT GCA CCG      864
253 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
254      275                     280                     285
256 GTG TTC GCG CGC CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC      912
257 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
258      290                     295                     300
260 GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA      960

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/08/900,220C

DATE: 11/28/2000  
 TIME: 11:51:02

Input Set : A:\ONV-044.01 SeqList.txt  
 Output Set: N:\CRF3\11282000\H900220C.raw

```

261 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
262 305          310          315          320
264 GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC      1008
265 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
266          325          330          335
268 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG      1056
269 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
270          340          345          350
271 GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT      1104
272 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
273          355          360          365
275 CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT      1152
276 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
277          370          375          380
279 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG      1190
280 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
281 385          390          395

284 (2) INFORMATION FOR SEQ ID NO: 3:
286 (i) SEQUENCE CHARACTERISTICS:
287 (A) LENGTH: 1281 base pairs
288 (B) TYPE: nucleic acid
289 (C) STRANDEDNESS: both
290 (D) TOPOLOGY: linear
292 (ii) MOLECULE TYPE: cDNA
295 (ix) FEATURE:
296 (A) NAME/KEY: CDS
297 (B) LOCATION: 1..1233
299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
301 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG      48
302 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
303 1          5          10          15
305 CTG CTG CTG CTT CTG GTG CCG GCG GCG GGC TGC GGG CCG GGC CGG      96
306 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
307          20          25          30
309 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC      144
310 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
311          35          40          45
313 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC      192
314 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
315          50          55          60
317 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG      240
318 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
319          65          70          75          80
321 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC      288
322 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
323          85          90          95
325 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC      336
326 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
327          100          105          110

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← F.Y.I.

VERIFICATION SUMMARY                      DATE: 11/28/2000  
PATENT APPLICATION:    US/08/900,220C        TIME: 11:51:03

Input Set : A:\ONV-044.01 SeqList.txt  
Output Set: N:\CRF3\11282000\H900220C.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:2249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2347 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=[nucleic acid]  
L:2363 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=[nucleic acid]  
L:2378 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25, Value=[nucleic acid]  
L:2409 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26, Value=[nucleic acid]  
L:2424 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27, Value=[nucleic acid]  
L:2439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28, Value=[nucleic acid]  
L:2453 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29, Value=[nucleic acid]  
L:2467 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30, Value=[nucleic acid]  
L:2481 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31, Value=[nucleic acid]  
L:2495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32, Value=[nucleic acid]